

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/820,777A
Source: IFW/6
Date Processed by STIC: 11/3/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 11/03/2006

PATENT APPLICATION: US/10/820,777A

TIME: 17:05:49

Input Set : A:\Third Amended Seq Listing 683884-2US.txt

Output Set: N:\CRF4\11032006\J820777A.raw

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2 <110> APPLICANT: Cheng, Winston T.K.
3   Chen, Chuan-Mu
4   Lin, Shwu-Wha
5   Wang, Chih-Hong
6   Lin, Chih-Jen
7   Wu, Shinn-Chih
9 <120> TITLE OF INVENTION: Method for producing biologically active human factor VIII
10   in the milk of transgenic animals driven by mammary-specific
11   expression cassettes
13 <130> FILE REFERENCE: 683884-2US
15 <140> CURRENT APPLICATION NUMBER: US 10/820,777A
16 <141> CURRENT FILING DATE: 2004-04-09
18 <160> NUMBER OF SEQ ID NOS: 15
20 <170> SOFTWARE: PatentIn version 3.2
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 63
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Synthetic
30 <400> SEQUENCE: 1
31 atgatgtcct ttgtctctct gtcctcggtta ggcatactat tccatgccac ccaggctggt      60
33 aac                                                                    63
36 <210> SEQ ID NO: 2
37 <211> LENGTH: 50
38 <212> TYPE: DNA
39 <213> ORGANISM: Artificial
41 <220> FEATURE:
42 <223> OTHER INFORMATION: Synthetic
44 <400> SEQUENCE: 2
45 atgaaacttc tcatacttac ctgtcttggt gctgttgctg ccaggttaac      50
48 <210> SEQ ID NO: 3
49 <211> LENGTH: 22
50 <212> TYPE: DNA
51 <213> ORGANISM: Homo sapiens
53 <400> SEQUENCE: 3
54 ggttaactgc caccagaaga ta      22
57 <210> SEQ ID NO: 4
58 <211> LENGTH: 20
59 <212> TYPE: DNA
60 <213> ORGANISM: Homo sapiens
62 <400> SEQUENCE: 4
63 aagcttcttg gttcaatggc      20

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66 <210> SEQ ID NO: 5
67 <211> LENGTH: 25
68 <212> TYPE: DNA
69 <213> ORGANISM: Homo sapiens
71 <400> SEQUENCE: 5
72 aagcttgaaa cgccatcaac gggaa 25
75 <210> SEQ ID NO: 6
76 <211> LENGTH: 24
77 <212> TYPE: DNA
78 <213> ORGANISM: Homo sapiens
80 <400> SEQUENCE: 6
81 ctcgagcctc agtagaggtc ctgt 24
84 <210> SEQ ID NO: 7
85 <211> LENGTH: 20
86 <212> TYPE: DNA
87 <213> ORGANISM: Homo sapiens
89 <400> SEQUENCE: 7
90 ctctcttgtc atcctcttcc 20
93 <210> SEQ ID NO: 8
94 <211> LENGTH: 21
95 <212> TYPE: DNA
96 <213> ORGANISM: Homo sapiens
98 <400> SEQUENCE: 8
99 ggttacgcgt caagattctg a 21
102 <210> SEQ ID NO: 9
103 <211> LENGTH: 20
104 <212> TYPE: DNA
105 <213> ORGANISM: Homo sapiens
107 <400> SEQUENCE: 9
108 agacttttcgg aacagaggca 20
111 <210> SEQ ID NO: 10
112 <211> LENGTH: 22
113 <212> TYPE: DNA
114 <213> ORGANISM: Homo sapiens
116 <400> SEQUENCE: 10
117 atcttttttcc aggtcaacat ca 22
120 <210> SEQ ID NO: 11
121 <211> LENGTH: 23
122 <212> TYPE: DNA
123 <213> ORGANISM: Homo sapiens
125 <400> SEQUENCE: 11
126 cattctattc atttcagtgg aca 23
129 <210> SEQ ID NO: 12
130 <211> LENGTH: 22
131 <212> TYPE: DNA
132 <213> ORGANISM: Homo sapiens
134 <400> SEQUENCE: 12
135 gagatgtaga ggctggagaa ct 22
138 <210> SEQ ID NO: 13

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139 <211> LENGTH: 19
140 <212> TYPE: PRT
141 <213> ORGANISM: Bovine
143 <400> SEQUENCE: 13
144 Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His
145           5                      10                      15
146 Ala Thr Glu Ala
149 <210> SEQ ID NO: 14
150 <211> LENGTH: 15
151 <212> TYPE: PRT
152 <213> ORGANISM: Bovine
154 <400> SEQUENCE: 14
155 Met Lys Leu Leu Ile Leu Thr Cys Leu Val Ala Val Ala Ala Arg
156           5                      10                      15
159 <210> SEQ ID NO: 15
160 <211> LENGTH: 1448
161 <212> TYPE: PRT
162 <213> ORGANISM: Artificial
164 <220> FEATURE:
165 <223> OTHER INFORMATION: Bovine-Homo sapiens fusion protein
167 <400> SEQUENCE: 15
168 Met Lys Leu Leu Ile Leu Thr Cys Leu Val Ala Val Ala Ala Arg Leu
169           5                      10                      15
170 Thr Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser
171           20                      25                      30
172 Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
173           35                      40                      45
174 Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
175           50                      55                      60
176 Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
177           65                      70                      75
178 Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
179           80                      85                      90
180 Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
181 95                      100                      105                      110
182 His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
183           115                      120                      125
184 Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
185           130                      135                      140
186 Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
187           145                      150                      155
188 Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
189           160                      165                      170
190 Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
191 175                      180                      185                      190
192 Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
193           195                      200                      205
194 Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
195           210                      215                      220

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196 Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
197      225      230      235
198 Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
199      240      245      250
200 Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
201 255      260      265      270
202 Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
203      275      280      285
204 Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
205      290      295      300
206 Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
207      305      310      315
208 Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
209      320      325      330
210 Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
211 335      340      345      350
212 Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
213      355      360      365
214 Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
215      370      375      380
216 Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
217      385      390      395
218 Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
219      400      405      410
220 Leu Val Leu Ala Pro Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
221 415      420      425      430
222 Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
223      435      440      445
224 Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
225      450      455      460
226 Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
227      465      470      475
228 Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
229      480      485      490
230 His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
231 495      500      505      510
232 Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
233      515      520      525
234 Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
235      530      535      540
236 Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
237      545      550      555
238 Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
239      560      565      570
240 Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
241 575      580      585      590
242 Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
243      595      600      605
244 Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp

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245		610		615		620
246	Pro Glu Phe	Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val				
247		625		630		635
248	Phe Asp Ser	Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp				
249		640		645		650
250	Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe					
251	655		660		665	670
252	Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr					
253		675		680		685
254	Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro					
255		690		695		700
256	Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly					
257		705		710		715
258	Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp					
259		720		725		730
260	Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys					
261	735		740		745	750
262	Asn Asn Ala Ile Glu Pro Arg Ser Leu Lys Arg His Gln Arg Glu Ile					
263		755		760		765
264	Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp					
265		770		775		780
266	Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu					
267		785		790		795
268	Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg His Tyr					
269		800		805		810
270	Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser Ser Ser					
271	815		820		825	830
272	Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val Pro Gln Phe					
273		835		840		845
274	Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro					
275		850		855		860
276	Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr					
277		865		870		875
278	Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln					
279		880		885		890
280	Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu					
281	895		900		905	910
282	Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe Val Lys Pro Asn					
283		915		920		925
284	Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His Met Ala Pro Thr					
285		930		935		940
286	Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp Val Asp					
287		945		950		955
288	Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu Val Cys					
289		960		965		970
290	His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln					
291	975		980		985	990
292	Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr					
293		995		1000		1005

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/03/2006
PATENT APPLICATION: US/10/820,777A TIME: 17:05:50

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,15

VERIFICATION SUMMARY

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